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**RAW SEQUENCE LISTING**

DATE: 03/19/2003

PATENT APPLICATION: US/09/612,925D

TIME: 11:57:41

Input Set : N:\Crf3\RULE60\09612925.raw.txt

Output Set: N:\CRF4\03192003\I612925D.raw

**SEQUENCE LISTING**

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: DUARTE CANO, C. A.

6 GUILL N NIETO, G. E.

7 MART N DUNN, A. M.

8 ALVAREZ ACOSTA, A.

9 CARPIO MUÑOZ, E. L.

10 QUINTANA V. D.

11 G MEZ RODR GUEZ, C. E.

12 SILVA RODR GUEZ, R. C.

13 NAZ BAL G LVEZ, C.

14 LEAL ANGULO, M. J.

16 (ii) TITLE OF INVENTION: System for the expression of heterologous  
17 antigens as fusion proteins

19 (iii) NUMBER OF SEQUENCES: 21

21 (iv) CORRESPONDENCE ADDRESS:

22 (A) ADDRESSEE: Lackenbach Siegel Marzullo Aronson &amp; Greenspan

23 (B) STREET: One Chase Road

24 (C) CITY: Scarsdale

25 (D) STATE: New York

26 (E) COUNTRY: U.S.

27 (F) ZIP: 10583

29 (v) COMPUTER READABLE FORM:

30 (A) MEDIUM TYPE: Floppy disk 3.5'' (1.4 MB).

31 (B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).

32 (C) OPERATING SYSTEM: Windows 95.

33 (D) SOFTWARE: Word Perfect 5.0 for Windows 95.

35 (vi) CURRENT APPLICATION DATA:

C--&gt; 36 (A) APPLICATION NUMBER: US/09/612,925D

C--&gt; 37 (B) FILING DATE: 10-Jul-2000

W--&gt; 43 (C) CLASSIFICATION: 435

40 (vii) PRIOR APPLICATION DATA:

41 (A) APPLICATION NUMBER: US/08/930,917A

42 (B) FILING DATE: 16-Sep-1997

44 (A) APPLICATION NUMBER: PCT/CU97/00001

45 (B) FILING DATE: 17-Jan-1997

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: HENRY A. MARZULLO, JR.

49 (B) REGISTRATION NUMBER: 20,910

50 (C) REFERENCE/DOCKET NUMBER: P-13

52 (ix) TELECOMMUNICATION INFORMATION:

53 (A) TELEPHONE: (914) 723-4300

54 (B) TELEFAX: (914) 723-4301

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## 57 (2) INFORMATION FOR SEQ ID NO: 1:

## 59 (i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 47 Amino acid residues

61 (B) TYPE: Amino acid

62 (C) STRANDEDNESS: Unknown

63 (D) TOPOLOGY: Unknown

65 (ii) MOLECULE TYPE: Peptide

67 (iii) HYPOTHETICAL: No

69 (iv) ANTI-SENSE: No

W--> 71 (v) **FRAGMENT TYPE: -N Terminal fragment**

73 (vi) ORIGINAL SOURCE:

74 (A) ORGANISM: Neisseria meningitidis

75 (B) STRAIN: B:4:P1.15

77 (vii) IMMEDIATE SOURCE:

78 (A) LIBRARY: Genomic

79 (B) CLONE: P64K

81. (ix) FEATURE:

82 (D) OTHER INFORMATION: First 47 amino acids of the recombinant protein

83 of Neisseria meningitidis P64K.

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

86 Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

87 1 5 10 15

88 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

89 20 25 30

90 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp

91 35 40 45

## 93 (2) INFORMATION FOR SEQ ID NO: 2:

## 94 (i) SEQUENCE CHARACTERISTICS:

95 (A) LENGTH: 29 base pairs

96 (B) TYPE: Nucleic acid

97 (C) STRANDEDNESS: Unknown

98 (D) TOPOLOGY: Unknown

100 (ii) MOLECULE TYPE: Other nucleic acid

101 (A) DESCRIPTION: Synthetic oligonucleotide

103 (iii) HYPOTHETICAL: No.

105 (iv) ANTI-SENSE: No

W--> 107 (v) **FRAGMENT TYPE: -N Terminal fragment**

109 (vi) ORIGINAL SOURCE:

110 (A) ORGANISM: Neisseria meningitidis

111 (B) STRAIN: B:4:P1.15

113 (vii) IMMEDIATE SOURCE:

114 (A) LIBRARY: Genomic

115 (B) CLONE: P64K

117 (ix) FEATURE:

118 (A) NAME/KEY: 1573

119 (D) OTHER INFORMATION: Primer 5' for PCR amplification of the first

120 44 amino acids of the recombinant protein of Neisseria

121 meningitidis P64K.

123 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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124  
TTCCATGGTA GATAAAAGAA TGGCTTTAG 29

126 (2) INFORMATION FOR SEQ ID NO: 3:  
128 (i) SEQUENCE CHARACTERISTICS:  
129 (A) LENGTH: 29 base pairs  
130 (B) TYPE: Nucleic acid  
131 (C) STRANDEDNESS: Unknown  
132 (D) TOPOLOGY: Unknown  
134 (ii) MOLECULE TYPE: Other nucleic acid  
135 (A) DESCRIPTION: Synthetic oligonucleotide  
137 (iii) HYPOTHETICAL: No.  
139 (iv) ANTI-SENSE: No  
W--> 141 (v) **FRAGMENT TYPE: -C Terminal fragment**  
142 (vi) ORIGINAL SOURCE:  
143 (A) ORGANISM: Neisseria meningitidis  
144 (B) STRAIN: B:4:P1.15  
146 (vii) IMMEDIATE SOURCE:  
147 (A) LIBRARY: Genomic  
148 (B) CLONE: P64K  
150 (ix) FEATURE:  
151 (A) NAME/KEY: 1575  
152 (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first  
153 47 amino acids of the recombinant protein of Neisseria  
154 meningitidis P64K.  
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
157 TTTCTAGATC CAAAGTAATC AGGGTATCG 29  
159 (2) INFORMATION FOR SEQ ID NO: 4:  
161 (i) SEQUENCE CHARACTERISTICS:  
162 (A) LENGTH: 26 base pairs  
163 (B) TYPE: Nucleic acid  
164 (C) STRANDEDNESS: Unknown  
165 (D) TOPOLOGY: Unknown  
167 (ii) MOLECULE TYPE: Other nucleic acid  
168 (A) DESCRIPTION: Synthetic oligonucleotide  
170 (iii) HYPOTHETICAL: No  
172 (iv) ANTI-SENSE: No  
W--> 174 (v) **FRAGMENT TYPE: -C Terminal fragment**  
176 (vi) ORIGINAL SOURCE:  
177 (A) ORGANISM: Neisseria meningitidis  
178 (B) STRAIN: B:4:P1.15  
180 (vii) IMMEDIATE SOURCE:  
181 (A) LIBRARY: Genomic  
182 (B) CLONE: P64K  
184 (ix) FEATURE:  
185 (A) NAME/KEY: Primer 2192  
186 (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first  
187 120 amino acids of the recombinant protein of Neisseria  
188 meningitidis P64K  
190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
191 GGCGGTTCTG CCGATTAAGG ATCCGA 26

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## 193 (2) INFORMATION FOR SEQ ID NO: 5:

## 195 (i) SEQUENCE CHARACTERISTICS:

196 (A) LENGTH: 146 base pairs

197 (B) TYPE: Nucleic acid

198 (C) STRANDEDNESS: Unknown

199 (D) TOPOLOGY: Unknown

## 201 (ii) MOLECULE TYPE: Other nucleic acid

202 (A) DESCRIPTION: Fragment amplified by PCR

## 204 (iii) HYPOTHETICAL: Yes

## 206 (iv) ANTI-SENSE: No

## 208 (v) FRAGMENT TYPE: -N-terminal fragment

## 210 (vi) ORIGINAL SOURCE:

211 (A) ORGANISM: Neisseria meningitidis

212 (B) STRAIN: B:4:P1.15

## 214 (vii) IMMEDIATE SOURCE:

215 (A) LIBRARY: Genomic

216 (B) CLONE: P64K

## 218 (ix) FEATURE:

219 (D) OTHER INFORMATION: Fragment derived from the first 47 amino acids

220 of the recombinant protein of Neisseria meningitidis P64K,

221 containing a NcoI site at the position 3 to 8 and a XbaI site

222 at the position 139 to 144

## 224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

225	TTCCATGGTA	GATAAAAGAA	TGGCTTTAGT	TGAATTGAAA	GTGCCCGACA	TTGGCGGACA	60
227	CGAAAAATGTA	GATATTATCG	CGGTTGAAGT	AAACGTGGGC	GACACTATTG	CTGTGGACGA	120
229	TACCCTGATT	ACTTTGGATC	TAGAAA			146	

## 232 (2) INFORMATION FOR SEQ ID NO: 6:

## 234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 47 Amino acid residues

236 (B) TYPE: Amino acid

237 (C) STRANDEDNESS: Unknown

238 (D) TOPOLOGY: Unknown

## 240 (ii) MOLECULE TYPE: Peptide

## 242 (iii) HYPOTHETICAL: No

## 244 (iv) ANTI-SENSE: No

## W--&gt; 246 (v) FRAGMENT TYPE: -N Terminal fragment

## 248 (vi) ORIGINAL SOURCE:

249 (A) ORGANISM: Neisseria meningitidis

250 (B) STRAIN: B:4:P1.15

## 252 (vii) IMMEDIATE SOURCE:

253 (A) LIBRARY: Genomic

254 (B) CLONE: P64K

## 256 (ix) FEATURE:

257 (D) OTHER INFORMATION: Stabilizer derived from the first 47 amino

258 acids of the recombinant protein of Neisseria meningitidis P64K,

259 containing the following changes: L2 V2; E45 D45; T46 L46; D47 E47.

## 261 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

262	Met	Val	Asp	Lys	Arg	Met	Ala	Leu	Val	Glu	Leu	Lys	Val	Pro	Asp	Ile
263	1					5					10					15

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264 Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly  
 265                   20                   25                   30

266 Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu  
 267           35                   40                   45

269 (2) INFORMATION FOR SEQ ID NO: 7:

271 (i) SEQUENCE CHARACTERISTICS:

272 (A) LENGTH: 16 base pairs

273 (B) TYPE: Nucleic acid

274 (C) STRANDEDNESS: Unknown

275 (D) TOPOLOGY: Unknown

276 (ii) MOLECULE TYPE: Other nucleic acid

277 (A) DESCRIPTION: Synthetic oligonucleotide

279 (iii) HYPOTHETICAL: No.

281 (iv) ANTI-SENSE: No

W--> 283 (v) **FRAGMENT TYPE: -N Terminal fragment**

285 (vi) ORIGINAL SOURCE:

286 (A) ORGANISM: Neisseria meningitidis

287 (B) STRAIN: B:4:P1.15

289 (vii) IMMEDIATE SOURCE:

290 (A) LIBRARY: Genomic

291 (B) CLONE: P64K

293 (ix) FEATURE:

294 (A) NAME/KEY: 1576

295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

296 CTAGATTGGA TATCAG

16

298 (2) INFORMATION FOR SEQ ID NO: 8:

300 (i) SEQUENCE CHARACTERISTICS:

301 (A) LENGTH: 16 base pairs

302 (B) TYPE: Nucleic acid

303 (C) STRANDEDNESS: Unknown

304 (D) TOPOLOGY: Unknown

306 (ii) MOLECULE TYPE: Other nucleic acid

307 (A) DESCRIPTION: Synthetic oligonucleotide

309 (iii) HYPOTHETICAL: No

311 (iv) ANTI-SENSE: No

W--> 313 (v) **FRAGMENT TYPE: -N Terminal fragment**

315 (vi) ORIGINAL SOURCE:

316 (A) ORGANISM: Neisseria meningitidis

317 (B) STRAIN: B:4:P1.15

319 (vii) IMMEDIATE SOURCE:

320 (A) LIBRARY: Genomic

321 (B) CLONE: P64K

323 (ix) FEATURE:

324 (A) NAME/KEY: 1577

326 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

327 GATCCTGATA TCAAAT

16

329 (2) INFORMATION FOR SEQ ID NO: 9:

331 (i) SEQUENCE CHARACTERISTICS:

332 (A) LENGTH: 15 Amino acid residues

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 03/19/2003  
PATENT APPLICATION: US/09/612,925D      TIME: 11:57:42

Input Set : N:\Crf3\RULE60\09612925.raw.txt  
Output Set: N:\CRF4\03192003\I612925D.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 124

Seq#:5; Line(s) 225,227

Seq#:21; Line(s) 739,741,745,747,749

## VERIFICATION SUMMARY

DATE: 03/19/2003

PATENT APPLICATION: US/09/612,925D

TIME: 11:57:42

Input Set : N:\Crf3\RULE60\09612925.raw.txt

Output Set: N:\CRF4\03192003\I612925D.raw

L:36 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:37 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:43 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)  
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1  
L:107 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2  
L:141 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3  
L:174 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4  
L:246 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6  
L:283 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7  
L:313 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8  
L:571 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:571 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=17  
L:571 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17  
L:598 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:598 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=18  
L:598 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18  
L:640 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:640 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=19  
L:640 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19  
L:685 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:685 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=20  
L:685 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20  
L:734 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]  
L:734 M:238 W: Alpha Fields not Ordered, Reordered [(D) TOPOLOGY:] of (2)(i)  
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=21  
L:734 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21